GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 01:07:04 ; Search time 755.06 Seconds
(without alignments)
28.386 Million cell updates/sec

Title: US-09-851-670-19
Perfect score: 25
Sequence: 1 gctcgatctgtgatcccttctttgc 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101:*
1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
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10: /SIDS2/gcgdata/geneseq/geneseqn/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
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13: /SIDS2/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	15	60.0	60	20	AAX15696	PCR primer used to
2	14.6	58.4	22	22	AAF90964	Human multi drug r
3	14.6	58.4	22	22	AAF91062	Human multi drug r
4	14.4	57.6	33	21	AAZ58165	Human saposin A 5'
5	14.2	56.8	30	16	AAQ75842	Sense primer to am
c 6	14.2	56.8	47	21	AAZ69514	Human map-related
7	14	56.0	23	18	AAT89102	E. coli serotype 0
c 8	14	56.0	30	14	AAQ38554	T cell receptor PC
c 9	14	56.0	30	20	AAX02255	T cell receptor PC
c 10	14	56.0	31	21	AAZ96703	T cell antigen rec
11	14	56.0	40	22	AAF27353	PCR primer, SEQ ID
12	13.8	55.2	47	16	AAQ75515	Human hepatitis B
13	13.8	55.2	60	21	AAA91904	PCR primer #2 for
c 14	13.4	53.6	24	21	AAA27817	North American PRR
15	13.4	53.6	30	21	AAA37454	Arabidopsis acyltr
c 16	13.4	53.6	32	19	AAV49367	Primer AB152 for T
c 17	13.2	52.8	24	20	AAZ21385	Recombinant HIV-1
c 18	13.2	52.8	30	13	AAQ25323	5' PCR primer for
c 19	13.2	52.8	34	21	AAZ29698	Domain 1, 2 PCR(12
c 20	13.2	52.8	36	17	AAT10347	CAEV env gene TM f
21	13.2	52.8	37	21	AAA87335	Rat hepatocyte car
22	13	52.0	26	21	AAC81602	Pan-fungal rRNA/rD
23	13	52.0	26	22	AAC88473	Helper oligonuclot
24	13	52.0	26	22	AAC83425	Methoxy helper oli
25	13	52.0	26	22	AAC83602	Pan-fungal helper
c 26	13	52.0	27	21	AAA62797	Endoglucanase prim
c 27	13	52.0	30	17	AAT27103	Yeast calcineurin-
28	13	52.0	40	16	AAQ80091	ADPGPP large subun
29	13	52.0	40	16	AAQ85020	Primer for ADP-glu
c 30	13	52.0	43	22	AAD13157	Human membrane-typ
31	13	52.0	43	22	AAD13159	Human membrane-typ
c 32	13	52.0	46	20	AAX03233	PCR primer used to
33	13	52.0	50	22	AAD03101	1467-13 oligonucle
34	13	52.0	60	22	AAF85484	Nucleotide sequenc
35	13	52.0	60	22	AAF85488	Nucleotide sequenc
36	12.8	51.2	20	20	AAX96544	PCR primer used to
37	12.8	51.2	27	18	AAT86066	Primer P13b, used
38	12.8	51.2	30	22	AAD02148	P. funiculosum his
c 39	12.8	51.2	36	20	AAX78174	Selex procedure gr
c 40	12.8	51.2	37	20	AAX78175	Selex procedure gr
41	12.8	51.2	40	21	AAZ95762	Polynucleotide seq
42	12.8	51.2	41	17	AAT05803	Semliki forest vir
c 43	12.8	51.2	44	17	AAT05804	Human transferrin
44	12.8	51.2	47	21	AAZ68740	Human map-related
c 45	12.8	51.2	54	18	AAX73390	Mouse flk-1 VEGF r

ALIGNMENTS

RESULT 1
AAX15696
ID AAX15696 standard; DNA; 60 BP.
XX
AC AAX15696;
XX
DT 07-MAY-1999 (first entry)
XX
DE PCR primer used to amplify a protein phosphatase gene.
XX
KW Protein phosphatase gene; growth; fermentation activity;
KW dough production; yeast; PCR primer; ss.
XX
OS Synthetic.
OS Saccharomyces cerevisiae.
XX
PN JP11042090-A.
XX
PD 16-FEB-1999.
XX
PF 29-JUL-1997; 97JP-0203652.
XX
PR 29-JUL-1997; 97JP-0203652.
XX
PA (KANF) KANEKA CORP.
PA (SHOS) SHOWA SANGYO CO.
XX
DR WPI; 1999-197822/17.
XX
PT New yeast of controlled activation at low temperatures - useful for
PT improving the quality of dough
XX
PS Example 1; Page 10; 41pp; Japanese.
XX

```
CC   The present sequence represents a primer used to amplify DNA
CC   encoding protein phosphatase gene of Saccharomyces cerevisiae.
CC   The specification describes new S. cerevisiae in which the growth
CC   and/or the fermentation activity is controlled at least in the
CC   range of 0-20 degrees Celsius. These yeast are prepared by
CC   deleting the function of at least one protein phosphatase gene.
CC   The yeast is useful in the production of dough.
XX
SQ   Sequence 60 BP; 14 A; 15 C; 9 G; 22 T; 0 other;


  Query Match            60.0%;  Score 15;  DB 20;  Length 60;
  Best Local Similarity  78.3%;  Pred. No. 6.1e+02;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      3 tcgatctgtgatcccttctttgc 25
          || ||||  || ||||||||| ||
Db     11 tcaatcttggaacccttcttcgc 33


RESULT   2
AAF90964
ID   AAF90964 standard; DNA; 22 BP.
XX
AC   AAF90964;
XX
DT   04-MAY-2001  (first entry)
XX
DE   Human multi drug resistance-1 gene related sequence SEQ ID NO: 51.
XX
KW   Human; MDR-1; multi drug resistance-1; drug uptake; disease; cancer;
KW   inflammatory disease; neuronal disease; CNS disease;
KW   cardiovascular disease; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200109183-A2.
XX
PD   08-FEB-2001.
XX
PF   28-JUL-2000; 2000WO-EP07314.
XX
PR   30-JUL-1999;   99EP-0114938.
PR   22-FEB-2000; 2000EP-0103361.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI   Brinkmann U,  Hoffmeyer S,  Eichelbaum M,  Roots I;
XX
DR   WPI; 2001-159855/16.
XX
PT   New polynucleotide encoding a molecular variant Multi Drug Resistance
PT   (MDR)-1 polypeptide is useful for diagnosing and treating diseases
PT   associated with abnormal MDR-1 expression or function, e.g. cancer -
XX
PS   Claim 36; Page 87; 154pp; English.
XX
CC   The present invention provides nucleotides encoding molecular variants of
CC   the human multi drug resistance-1 (MDR-1) protein. These can be used to
CC   identify compounds capable of treating multidrug resistance and
CC   sensitivity interfering resulting from polymorphisms in MDR-1, which can
CC   lead to difficulties in treating cancer, cardiovascular, neuronal,
CC   inflammatory and CNS diseases.
XX
SQ   Sequence 22 BP; 4 A; 4 C; 4 G; 10 T; 0 other;


  Query Match            58.4%;  Score 14.6;  DB 22;  Length 22;
  Best Local Similarity  81.0%;  Pred. No. 8.1e+02;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      5 gatctgtgatcccttctttgc 25
          |||||||||  | ||| ||| |
Db      1 gatctgtgaactcttgttttc 21


RESULT   3
AAF91062
ID   AAF91062 standard; DNA; 22 BP.
XX
AC   AAF91062;
XX
DT   04-MAY-2001  (first entry)
XX
DE   Human multi drug resistance-1 gene related sequence SEQ ID NO: 149.
XX
KW   Human; MDR-1; multi drug resistance-1; drug uptake; disease; cancer;
KW   inflammatory disease; neuronal disease; CNS disease;
KW   cardiovascular disease; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200109183-A2.
XX
PD   08-FEB-2001.
XX
PF   28-JUL-2000; 2000WO-EP07314.
XX
PR   30-JUL-1999;   99EP-0114938.
PR   22-FEB-2000; 2000EP-0103361.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI   Brinkmann U,  Hoffmeyer S,  Eichelbaum M,  Roots I;
XX
DR   WPI; 2001-159855/16.
XX
PT   New polynucleotide encoding a molecular variant Multi Drug Resistance
PT   (MDR)-1 polypeptide is useful for diagnosing and treating diseases
PT   associated with abnormal MDR-1 expression or function, e.g. cancer -
XX
PS   Claim 36; Page 107; 154pp; English.
XX
CC   The present invention provides nucleotides encoding molecular variants of
CC   the human multi drug resistance-1 (MDR-1) protein. These can be used to
CC   identify compounds capable of treating multidrug resistance and
CC   sensitivity interfering resulting from polymorphisms in MDR-1, which can
CC   lead to difficulties in treating cancer, cardiovascular, neuronal,
CC   inflammatory and CNS diseases.
XX
SQ   Sequence 22 BP; 4 A; 4 C; 4 G; 10 T; 0 other;


  Query Match            58.4%;  Score 14.6;  DB 22;  Length 22;
  Best Local Similarity  81.0%;  Pred. No. 8.1e+02;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      5 gatctgtgatcccttctttgc 25
          |||||||||  | ||| ||| |
Db      1 gatctgtgaactcttgttttc 21


RESULT   4
AAZ58165
ID   AAZ58165 standard; DNA; 33 BP.
XX
AC   AAZ58165;
XX
DT   25-APR-2000  (first entry)
XX
DE   Human saposin A 5' PCR primer.
XX
KW   Saposin A; antiangiogenic; angiogenesis inhibitor; antitumour;
KW   antiproliferative; antimigratory; Kaposi's sarcoma; tumour; human;
KW   therapy; PCR primer; ss.
XX
```

OS Homo sapiens.
XX
PN WO200002902-A1.
XX
PD 20-JAN-2000.
XX
PF 12-JUL-1999; 99WO-US15772.
XX
PR 13-JUL-1998; 98US-0092647.
XX
PA (GILL/) GILL P S.
XX
PI Gill PS;
XX
DR WPI; 2000-171128/15.
XX
PT Saposin B derived peptides, useful as inhibitors of angiogenesis and
PT tumor growth -
XX
PS Example 1; Page 47; 78pp; English.
XX
CC The present sequence is that of a 5' primer used in the PCR
CC amplification of human saposin A cDNA using T1 fibroblast cell cDNA
CC as template. The primer pair (see also AAZ58166) was designed to
CC introduce a 5' XbaI site and a 3' XhoI site into the amplified
CC cDNA. The PCR product was cloned into bacterial and eukaryotic
CC expression vectors, for use in studies designed to determine
CC whether recombinant saposin B (see AAY58716) has antiangiogenic
CC activity. The invention is based on the discovery of the
CC antiangiogenic activity of saposin B. Small polypeptides (see
CC AAY58684-715) based on saposin B can be used for the treatment of
CC undesired angiogenesis and tumour growth, especially for the
CC treatment of Kaposi's sarcoma.
XX
SQ Sequence 33 BP; 8 A; 12 C; 4 G; 9 T; 0 other;

Query Match 57.6%; Score 14.4; DB 21; Length 33;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy      2 ctcgatctgtgatcccttctttgc 25
          || |||||   |||||||| |||
Db      1 ctagatctagaatcccttccctgc 24
```

RESULT 5
AAQ75842
ID AAQ75842 standard; DNA; 30 BP.
XX
AC AAQ75842;
XX
DT 18-AUG-1995 (first entry)
XX
DE Sense primer to amplify Non-A Non-B hepatitis virus for analysis.
XX
KW Non-A Non-B hepatitis virus; structural region; cDNA to genomic RNA;
KW detection; reagent; anti-Non-A Non-B hepatitis virus antibody;
KW vaccine; antigen; epitope; diagnosis; ss.
XX
OS Synthetic.
XX
PN EP628572-A.
XX
PD 14-DEC-1994.
XX
PF 27-MAY-1994; 94EP-0108256.
XX
PR 28-MAY-1993; 93JP-0126709.
PR 02-MAR-1994; 94JP-0032201.
XX
PA (ARIM/) ARIMA T.
PA (EISA) EISAI CO LTD.
XX
PI Aoyama M, Arima T, Hosoda T, Iwasaki Y, Obara T;
PI Sawada T, Tohmatsu J;
XX
DR WPI; 1995-015655/03.
XX
PT New non-A non-B hepatitis virus sub-type - used to develop prods.
PT for detection, diagnosis, prevention and treatment of non-A non-B
PT hepatitis.
XX
PS Example 2; Page 54; 59pp; English.
XX
CC This primer is based on nucleotides 6768-6787 of the Non-A Non-B
CC hepatitis virus strain HC-J8 genome encoding the non-structural protein.
CC It is used in conjunction with AAQ75843 to amplify nucleotides 2706-2496
CC of AAQ75818. The nucleotide sequences (see also AAQ75817-19) were
CC isolated from the plasma of donors in Japan with high s-GTP levels, and
CC were found to be different from previously reported NANB hepatitis
CC viruses. The DNA can be used as a reagent for detecting the NANB
CC hepatitis viral gene. The polypeptides can be used as reagents for
CC detecting anti-NANB hepatitis antibodies or as a NANB hepatitis viral
CC vaccine.
XX
SQ Sequence 30 BP; 4 A; 7 C; 10 G; 9 T; 0 other;

Query Match 56.8%; Score 14.2; DB 16; Length 30;
Best Local Similarity 84.2%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy      5 gatctgtgatcccttcttt 23
          || ||  ||||||||||||
Db      1 gagctcggatcccttcttt 19
```

RESULT 6
AAZ69514/c
ID AAZ69514 standard; DNA; 47 BP.
XX
AC AAZ69514;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related biallelic marker SEQ ID NO:3870.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(24,G)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium

PT map of the human genome -
XX
PS Claim 3; Page 1056; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 47 BP; 16 A; 9 C; 10 G; 12 T; 0 other;

Query Match 56.8%; Score 14.2; DB 21; Length 47;
Best Local Similarity 84.2%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 gatctgtgatcccttcttt 23
||||||||||||||||||||||
Db 23 GATCTGCGAGCCATTCTTT 5

RESULT 7
AAT89102
ID AAT89102 standard; DNA; 23 BP.
XX
AC AAT89102;
XX
DT 30-MAR-1998 (first entry)
XX
DE E. coli serotype 0157:H7 diagnostic fragment detecting PCR primer 5.
XX
KW Random amplified polymorphic DNA primer; RAPD primer;
KW microbe identification; microbe detection; PCR primer; ss.
XX
OS Synthetic.
OS Escherichia coli.
XX
PN WO9732043-A1.
XX
PD 04-SEP-1997.
XX
PF 24-FEB-1997; 97WO-US02831.
XX
PR 29-FEB-1996; 96US-0608881.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Jensen MA;
XX
DR WPI; 1997-448703/41.
XX
PT Identification of E. coli serotype 0157:H7 by detection of specific
PT DNA sequences - used for analysis of foods, clinical samples,
PT medical products etc.
XX
PS Claim 7; Page 17; 44pp; English.
XX
CC PCR primers AAT89098-104 are primers that have been identified as being
CC the most specific for the identification of Escherichia coli serotype
CC 0157:H7. They are derived from a highly specific diagnostic 1047 bp
CC fragment (AAT89095), as well as its complementary strand. AAT89098,
CC AAT89100, AAT89102, and AAT89104 are derived from AAT89095, while the
CC rest of the primers are derived from its complementary sequence. A number
CC of these primers, when used singly or in combination, resulted in several
CC other diagnostic PCR fragments (AAT89105-08) being identified. An
CC unknown microorganism is identified as a member of the E. coli 0157:H7
CC serotype if analysis of its genomic DNA indicates the presence of the
CC characteristic 1047 bp sequence or a diagnostic marker fragment of this
CC sequence. The method is used to detect cells of the 0147:H7 serotype in
CC foods, human or animal body fluids or tissues, environmental samples,
CC medical products and apparatus. The method is specific for the specified
CC serotype to the exclusion of all other bacteria, including other
CC serotypes of E. coli.
XX
SQ Sequence 23 BP; 5 A; 6 C; 4 G; 8 T; 0 other;

Query Match 56.0%; Score 14; DB 18; Length 23;
Best Local Similarity 77.3%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ctcgatctgtgatcccttcttt 23
||| ||||| || || | ||||
Db 1 ctcaatctgagagccgtacttt 22

RESULT 8
AAQ38554/c
ID AAQ38554 standard; DNA; 30 BP.
XX
AC AAQ38554;
XX
DT 16-JUL-1993 (first entry)
XX
DE T cell receptor PCR primer Vbeta15.
XX
KW Rheumatoid arthritis; synovial; therapy; therapeutic;
KW autoimmune response; variable region; mammal; immunisation;
KW polymerase chain reaction; ss.
XX
OS Synthetic.
XX
PN WO9304695-A.
XX
PD 18-MAR-1993.
XX
PF 27-AUG-1992; 92WO-US07289.
XX
PR 28-AUG-1991; 91US-0750913.
PR 06-JAN-1992; 92US-0817912.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
PA (WIST-) WISTAR INST.
XX
PI Weiner DB, Williams WV;
XX
DR WPI; 1993-100655/12.
XX
PT T-cell receptor based treatment of rheumatoid arthritis - comprises
PT administration of antibodies to T-cell receptor variable regions
XX
PS Disclosure; Fig 5; 110pp; English.
XX
CC The sequence is that of a human T cell receptor PCR primer, Vbeta15
CC which was used to amplify T cell receptor transcripts from cDNA
CC derived from rheumatoid synovial cell lines. It was used in
CC combination with the middle constant region primer (Cbeta-mid).
XX
SQ Sequence 30 BP; 13 A; 3 C; 8 G; 6 T; 0 other;

Query Match 56.0%; Score 14; DB 14; Length 30;
Best Local Similarity 77.3%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy      3 tcgatctgtgatcccttctttg 24
          || ||| | |||| || |||||
Db     30 TCCATCAGAGATCTCTCCTTTG 9


RESULT   9
AAX02255/c
ID   AAX02255 standard; DNA; 30 BP.
XX
AC   AAX02255;
XX
DT   06-MAY-1999  (first entry)
XX
DE   T cell receptor PCR primer V-beta 15.
XX
KW   T cell receptor; PCR primer; antigen-responsive T cell; population;
KW   disease; rheumatoid arthritis; Kawasaki disease; vaccine; infection;
KW   tumour; immunosuppression; therapy; pathogenic T cell overactivity; ss.
XX
OS   Synthetic.
XX
PN   WO9854223-A2.
XX
PD   03-DEC-1998.
XX
PF   27-MAY-1998;   98WO-GB01382.
XX
PR   27-MAY-1997;   97GB-0010820.
XX
PA   (UYDU-) UNIV DUNDEE.
XX
PI   Kay RA;
XX
DR   WPI; 1999-080808/07.
XX
PT   New method of identifying antigen-responsive T cells within T cell
PT   populations - useful in identifying specific T cell receptor types
PT   associated with particular diseases, including rheumatoid arthritis
PT   and Kawasaki disease
XX
PS   Disclosure; Fig 6; 76pp; English.
XX
CC   This invention describes a novel method for the identification of
CC   antigen-responsive T cells within T cell populations. The method
CC   comprises obtaining samples containing T cells that have responded to an
CC   antigen, and individually determining whether the expression of one or a
CC   number of genes, encoding a specific receptor or subset of T-cell
CC   receptors, is higher in samples containing T cells that have responded
CC   to the antigen, compared to samples containing T cells that have not.
CC   The method is useful in identifying specific antigen-responsive T cells
CC   or subsets of T cells involved in a given antigen response. Therefore,
CC   the method can identify a specific T cell receptor type associated with
CC   a particular disease, e.g. Rheumatoid arthritis or Kawasaki disease. The
CC   method enables the development of vaccines against infection and
CC   tumours, and allows specific targeting of immunosuppressive therapy
CC   towards diseases associated with pathogenic T cell overactivity.
CC   AAX02228-X02272 are PCR primers used in the method of the invention.
XX
SQ   Sequence 30 BP; 13 A; 3 C; 8 G; 6 T; 0 other;


  Query Match             56.0%;  Score 14;  DB 20;  Length 30;
  Best Local Similarity   77.3%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      3 tcgatctgtgatcccttctttg 24
          || ||| | |||| || |||||
Db     30 TCCATCAGAGATCTCTCCTTTG 9


RESULT  10
AAZ96703/c
ID   AAZ96703 standard; DNA; 31 BP.
XX
AC   AAZ96703;
XX
DT   11-APR-2000  (first entry)
XX
DE   T cell antigen receptor Vbeta chain DNA amplifying primer.
XX
KW   Rheumatoid arthritis; arthrosis deformans; T-cell antigen receptor;
KW   Vbeta chain; autoantigen; immunological tolerance; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9963084-A1.
XX
PD   09-DEC-1999.
XX
PF   28-MAY-1999;   99WO-JP02814.
XX
PR   29-MAY-1998;   98JP-0149855.
PR   14-OCT-1998;   98JP-0328761.
XX
PA   (TORI ) TORII PHARM CO LTD.
XX
PI   Nishioka K,  Yoshino S;
XX
DR   WPI; 2000-086978/07.
XX
PT   T-cell antigen receptor V-beta chain CDR3 region sequences accumulated
PT   in synovial membranes of rheumatoid arthritis patients  -
XX
PS   Example 1; Page 8; 136pp; Japanese.
XX
CC   The invention relates to peptide sequences present in the synovial fluid
CC   and membranes of rheumatoid arthritis patients, arising from the CDR
CC   region of oligoclonal pathogenic T-cell antigen receptor Vbeta chains.
CC   Compositions which contain autoantigenic peptides binding specifically
CC   to T-cells expressing receptors containing the peptide sequences, which
CC   include antigen-specific immunological tolerance to rheumatoid arthritis
CC   can be used for the treatment and prevention of rheumatoid arthritis.
CC   The invention can be used for the diagnosis, treatment and prevention
CC   of rheumatoid arthritis. Sequences AAZ96689-Z96730 represent primers
CC   for amplifying the DNA encoding the peptides from the various Vbeta
CC   chains of T cell antigen receptor.
XX
SQ   Sequence 31 BP; 11 A; 4 C; 8 G; 8 T; 0 other;


  Query Match             56.0%;  Score 14;  DB 21;  Length 31;
  Best Local Similarity   77.3%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      3 tcgatctgtgatcccttctttg 24
          || ||| | |||| || |||||
Db     31 TCCATCAGAGATCTCTCCTTTG 10


RESULT  11
AAF27353
ID   AAF27353 standard; DNA; 40 BP.
XX
AC   AAF27353;
XX
DT   24-APR-2001  (first entry)
XX
DE   PCR primer, SEQ ID NO:64, used in SIV-derived vector construction.
XX
KW   Retroviral vector; gene therapy vector; self-inactivating;
KW   Rev responsive element; RRE core sequence; SIV-derived vector
KW   simian immunodeficiency virus; PCR primer; ss.
XX
OS   Synthetic.
XX
```

PN WO200078987-A1.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-JP03955.
XX
PR 22-JUN-1999; 99JP-0175646.
XX
PA (DNAV-) DNAVEC RES INC.
XX
PI Nakajima T, Nakamaru K, Hasegawa M, Hayami M, Ido E;
XX
DR WPI; 2001-080832/09.
XX
PT Vector expressing two foreign genes and using a lentivirus Rev
PT responsive element, useful as a gene therapy vector -
XX
PS Example 5; Page 90; 105pp; Japanese.
XX
CC The invention relates to a novel retroviral vector which expresses two
CC foreign genes by using the Rev responsive element (RRE) core sequence.
CC The retrovirus-based vector contains the following components (in 5' to
CC 3' order):
CC (a) a viral expression regulatory sequence;
CC (b) a splicing donor sequence;
CC (c) the first foreign gene;
CC (d) an RRE core sequence;
CC (e) a splicing receptor sequence;
CC (f) the second foreign gene.
CC Alternatively, the vector can contain these components in the sequence
CC (a), (b), (d), (c), (e), and (f). The invention also encompasses a
CC method for the manufacture of the vector in packaging cells. The vector
CC is useful as a gene therapy vector for the transfer of two genes in which
CC their expression levels or expression level ratio is effectively
CC regulated. The vector is an efficient retroviral self-inactivating
CC vector in which the risk of recombination with wild-strain virus is
CC substantially reduced, and which does not express any viral structural
CC protein. The present sequence represents a PCR primer used in an
CC exemplification in the construction of a vector of the invention
CC based on SIV (simian immunodeficiency virus).
XX
SQ Sequence 40 BP; 6 A; 13 C; 8 G; 13 T; 0 other;

Query Match 56.0%; Score 14; DB 22; Length 40;
Best Local Similarity 77.3%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 cgatctgtgatccccttctttgc 25
|||||| | |||||||| ||
Db 19 cgatctttccgcccttcttggc 40

RESULT 12
AAQ75515
ID AAQ75515 standard; DNA; 47 BP.
XX
AC AAQ75515;
XX
DT 25-JUL-1995 (first entry)
XX
DE Human hepatitis B specific immunogen DNA.
XX
KW Human hepatitis B; HBV; surface antigen; immunogen; vaccine; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT mat_peptide 1..47
FT /*tag= a
XX
PN WO9426886-A.
XX
PD 24-NOV-1994.
XX
PF 05-MAY-1994; 94WO-IT00054.
XX
PR 11-MAY-1993; 93IT-0RM0301.
XX
PA (RICE-) IST RICERCHE BIOLOGIA MOLECOLARE ANGELETTI.
XX
PI Cortese R, Felici F, Luzzago A, Monaci P, Nicosia A;
XX
DR WPI; 1995-006783/01.
DR P-PSDB; AAR62572.
XX
PT Selecting immunogens and diagnostic reagents using phage
PT libraries - expressing oligopeptide(s) on the surface, useful
PT for vaccines, partic. against hepatitis virus and auto:immune
PT disease
XX
PS Claim 14; Page 29; 79pp; English.
XX
CC AAQ75513-Q75516 encode AAR62570-R62573, specific immunogens for the
CC disease caused by human hepatitis B virus (HBV). These peptides
CC mimic the HBV surface antigen (HBsAg), therefore when injected
CC into individuals not immune to HBV they elicit an immune response,
CC specifically the production of anti-HBsAg antibodies.
XX
SQ Sequence 47 BP; 4 A; 15 C; 13 G; 15 T; 0 other;

Query Match 55.2%; Score 13.8; DB 16; Length 47;
Best Local Similarity 88.2%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 tctgtgatcccttcttt 23
|||| | ||||||||||
Db 5 tctgcggtcccttcttt 21

RESULT 13
AAA91904
ID AAA91904 standard; DNA; 60 BP.
XX
AC AAA91904;
XX
DT 22-DEC-2000 (first entry)
XX
DE PCR primer #2 for amplification of exon 2 of PAH gene.
XX
KW PAH; phenylalanine hydroxylase; neuroleptic; psychotic; mood;
KW personality disorder; polymorphism; mutation; human; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200049160-A1.
XX
PD 24-AUG-2000.
XX
PF 17-FEB-2000; 2000WO-US02515.
XX
PR 19-FEB-1999; 99US-0253025.
XX
PA (NYME-) NEW YORK STATE OFFICE MENTAL HEALTH.
XX
PI Richardson MA;
XX
DR WPI; 2000-549275/50.
XX
PT Diagnosing psychotic disorders e.g. schizophrenia or detecting a person
PT at increased risk of developing such disorders, comprises detecting a
PT sequence alteration in phenylalanine hydroxylase genomic DNA -
XX
PS Claim 8; Page 25; 68pp; English.
XX

CC The present invention relates to the diagnosis of a pathophysiological
CC subtype of psychotic, mood or personality disorders or detecting a
CC person at increased risk of developing such disorders. The process
CC involves obtaining sample from the person and detecting a sequence
CC alteration in the phenylalanine hydroxylase (PAH) gene. Specifically,
CC the invention involves detection of a K274E mutation or an L321L
CC polymorphism. A composition of branched chain amino acids or aromatic
CC amino acids and normal PAH DNA is used for treating a person diagnosed
CC of having psychotic disorders or for preventing the development of such
CC disorders in first or second degree relatives of the subject. The
CC present sequence is a PCR primer used for amplification of part of the
CC coding region of the PAH gene.
XX
SQ Sequence 60 BP; 1 A; 33 C; 14 G; 12 T; 0 other;

Query Match 55.2%; Score 13.8; DB 21; Length 60;
Best Local Similarity 72.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 gctcgatctgtgatcccttctttgc 25
|| || ||||| || ||| ||||
Db 36 gcccgtcctgtgttcttttcattgc 60

RESULT 14
AAA27817/c
ID AAA27817 standard; DNA; 24 BP.
XX
AC AAA27817;
XX
DT 12-SEP-2000 (first entry)
XX
DE North American PRRS virus ORF1a primer RACE3.
XX
KW North American PRRS virus; Nidovirales virus; pig; swine; vaccine;
KW PCR primer; RACE; ss.
XX
OS North American porcine reproductive and respiratory syndrome virus.
XX
PN EP1018557-A2.
XX
PD 12-JUL-2000.
XX
PF 25-NOV-1999; 99EP-0309409.
XX
PR 22-DEC-1998; 98US-0113345.
XX
PA (PFIZ) PFIZER PROD INC.
XX
PI Calvert JG, Welch SW, Sheppard MG;
XX
DR WPI; 2000-444364/39.
XX
PT New polynucleotide encoding an infectious RNA molecule of a North
PT American porcine reproductive and respiratory syndrome virus for use as
PT a vaccine in protecting swine and other animals from infection by a
PT pathogen -
XX
PS Example 1; Page 17; 53pp; English.
XX
CC The present sequence is that of primer RACE3, complementary to
CC nucleotides 1733-1756 in the ORF1a gene of North American porcine
CC reproductive and respiratory syndrome (PRRS) virus P129A. It was
CC used in a 5' RACE to determine the extreme 5' end of the P129A
CC genome. cDNA corresponding to the North American PRRS virus genome
CC is given in AAA27809. The invention relates to polynucleotide
CC molecules, plasmids, viral vectors and transfected host cells that
CC comprise this DNA. It also relates to polynucleotide molecules,
CC viral vectors and transfected host cells encoding a genetically
CC modified North American PRRS virus that is disabled in its ability
CC to cause PRRS, or which encodes 1 or more heterologous antigenic
CC epitopes, for use as a vaccine.
XX
SQ Sequence 24 BP; 8 A; 3 C; 11 G; 2 T; 0 other;

Query Match 53.6%; Score 13.4; DB 21; Length 24;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 tgatcccttctttgc 25
||| ||||||||||||
Db 22 TGACCCCTTCTTTGC 8

RESULT 15
AAA37454
ID AAA37454 standard; DNA; 30 BP.
XX
AC AAA37454;
XX
DT 15-AUG-2000 (first entry)
XX
DE Arabidopsis acyltransferase ATAT5 5' RACE PCR primer, SEQ ID NO:143.
XX
KW Acyltransferase; lipid synthesis; recombinant expression;
KW membrane fluidity; cold resistance; transgenic plant;
KW rapid amplification of cDNA ends; RACE PCR primer; ss.
XX
OS Arabidopsis thaliana.
XX
PN WO200018889-A2.
XX
PD 06-APR-2000.
XX
PF 24-SEP-1999; 99WO-US22231.
XX
PR 25-SEP-1998; 98US-0101939.
XX
PA (CALJ) CALGENE LLC.
XX
PI Lassner MW, Emig RA, Ruezinsky DM, Van Eenennaam A;
XX
DR WPI; 2000-303447/26.
XX
PT Novel acyltransferase related proteins useful for altering membrane
PT fluidity in plant cells e.g. to induce chill tolerance -
XX
PS Example 5; Page 27; 126pp; English.
XX
CC The invention relates to nucleic acids encoding novel plant
CC acyltransferase-like proteins (AAA37343-A37445) which comprise one of 8
CC conserved acyltransferase motifs (AAY99474-Y99481). Acyltransferases
CC catalyse the transfer of acyl groups from a donor to a variety of
CC substrates such as glycerides, sterols, stanols and phosphatides.
CC Such enzymes play a key role in lipid synthesis, and thereby affect the
CC characteristics of the plant. For example, cold-hardened plants have
CC different lipid concentrations in the cell membrane compared to
CC non-hardened plants, which makes the membrane more fluid and the plant
CC more tolerant of low temperatures. The nucleic acid sequences of the
CC invention can be used as probes or for expressing acyltransferase-like
CC proteins in host cells e.g., for recombinant protein production. They
CC may be expressed in plant cells to alter the lipid composition of the
CC plant e.g., for the production of chill-resistant plants, or for altering
CC the composition of plant oils. Sequences AAA37446-A37471 represent RACE
CC (rapid amplification of cDNA ends) PCR primers used in an
CC exemplification of the invention to generate Arabidopsis thaliana
CC acyltransferase cDNA clones comprising the entire coding sequence.
XX
SQ Sequence 30 BP; 6 A; 4 C; 11 G; 9 T; 0 other;

Query Match 53.6%; Score 13.4; DB 21; Length 30;
Best Local Similarity 73.9%; Pred. No. 3e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy       3 tcgatctgtgatcccttctttgc 25
           |||| ||||||||  |  || ||
Db       1 tcgagctgtgatcgatgattggc 23
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